192

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4	22	100.0	258	9	HUMHCW12BA	L12954 Human MHC H
5	22	100.0	258	9	HUMHCW21BA	L12955 Human MHC H
6	22	100.0	258	9	HUMHCW22BA	L12956 Human MHC H
7	22	100.0	258	9	HUMHCW2B1A	L12952 Human MHC H
8	22	100.0	258	9	HUMHCW2B2A	L12953 Human MHC H
9	22	100.0	258	9	AF243536	AF243536 Homo sapi
10	22	100.0	262	9	HSU26659	U26659 Human MHC C
11	22	100.0	266	9	AF363727	AF363727 Homo sapi
12	22	100.0	267	9	AF239244	AF239244 Homo sapi
13	22	100.0	269	6	I27870	I27870 Sequence 42
14	22	100.0	269	6	I27871	I27871 Sequence 43
15	22	100.0	269	6	I27872	I27872 Sequence 44
16	22	100.0	269	6	I27873	I27873 Sequence 45
17	22	100.0	269	6	I27874	I27874 Sequence 46
18	22	100.0	269	9	HUMMHDRBAA	M62474 Human MHC c
19	22	100.0	270	9	AB007634	AB007634 Homo sapi
20	22	100.0	270	9	HSA293861	AJ293861 Homo sapi
21	22	100.0	270	9	HSGIPIHLA	Z72424 H.sapiens H
22	22	100.0	270	9	HUMMHDRA2E	M16958 Human MHC c
23	22	100.0	270	9	AF172070	AF172070 Homo sapi
24	22	100.0	285	9	AF010142	AF010142 Homo sapi
25	22	100.0	328	9	AF297459	AF297459 Homo sapi
26	22	100.0	338	9	AF373015	AF373015 Homo sapi
27	22	100.0	340	9	HUMMHDHOA	M30180 Human MHC c
28	22	100.0	350	9	AF439712	AF439712 Homo sapi
29	22	100.0	369	9	HUMMHRMNA	M30179 Human MHC c
30	22	100.0	407	9	AF335231	AF335231 Homo sapi
31	22	100.0	714	9	HUMMHDRA2D	M16957 Human MHC c
32	22	100.0	714	9	HUMMHDRA2F	M16959 Human MHC c
33	22	100.0	714	9	HUMMHDRBL	M17378 Human MHC c
34	22	100.0	826	9	HUMMHDR2A	L02545 Homo sapien
35	22	100.0	869	9	AF142469	AF142469 Homo sapi
36	22	100.0	885	9	AF142467	AF142467 Homo sapi
37	22	100.0	897	9	AF142468	AF142468 Homo sapi
38	22	100.0	1033	9	HUMMHCDW2C	M28583 Human (clon
39	22	100.0	1039	9	HUMMHDRGB	M20504 Human MHC c
40	22	100.0	1091	9	HUMMHCDW2D	M28584 Human (clon
41	22	100.0	1158	9	HUMMHDRWA	M20430 Human MHC c
42	21	95.5	248	9	AF191104	

has 192 & 222

Result No.		Score	% Query Match	Length	DB	ID	Description
1		19	100.0	20	6	AR020491	AR020491 Sequence
2		19	100.0	20	6	AR020498	AR020498 Sequence
3		19	100.0	20	6	AR051223	AR051223 Sequence
4		19	100.0	20	6	AR051230	AR051230 Sequence
5		19	100.0	20	6	AR053214	AR053214 Sequence
6		19	100.0	20	6	AR053221	AR053221 Sequence
7		19	100.0	20	6	AX001204	AX001204 Sequence
8		19	100.0	20	6	AX268628	AX268628 Sequence
9		19	100.0	23	6	A42459	A42459 Sequence 8
10		19	100.0	24	6	I28140	I28140 Sequence 31
c	11	19	100.0	69	6	AR097013	AR097013 Sequence
12		19	100.0	74	6	AR097014	AR097014 Sequence
c	13	19	100.0	152	9	HUMMHDHOB	M30182 Human MHC c
c	14	19	100.0	231	9	HSDNAHLAB	X75347 H.sapiens D
c	15	19	100.0	237	9	HSDRB13EX	X93315 H.sapiens H
c	16	19	100.0	238	9	AF011786	AF011786 Homo sapi
c	17	19	100.0	245	9	HSDRB1312	X82508 H.sapiens H
c	18	19	100.0	254	9	AF349316	AF349316 Homo sapi
c	19	19	100.0	255	9	HUMHLADRBZ	M84357 Human lymph
c	20	19	100.0	255	9	AF186407	AF186407 Homo sapi
c	21	19	100.0	255	9	AF186408	AF186408 Homo sapi
c	22	19	100.0	255	9	AF201762	AF201762 Homo sapi
c	23	19	100.0	255	9	AF339884	AF339884 Homo sapi
c	24	19	100.0	258	9	HUMHLDRB3G	L29807 Homo sapien
c	25	19	100.0	259	9	AF112877	AF112877 Homo sapi
c	26	19	100.0	260	9	HSU95818	U95818 Human MHC c
c	27	19	100.0	261	9	HSU36826	U36826 Human MHC c
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c	29	19	100.0	262	9	HSU26659	U26659 Human MHC C
c	30	19	100.0	262	9	HSU79026	U79026 Human isola
c	31	19	100.0	263	9	HSU34602	U34602 Human MHC c
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c	33	19	100.0	265	9	HUMHLADRBC	D17742 Human DNA f
c	34	19	100.0	266	9	AY042678	AY042678 Homo sapi
c	35	19	100.0	266	9	HSDRB1115	Z37161 H.sapiens D
c	36	19	100.0	266	9	HSHLA117	X82210 H.sapiens H
c	37	19	100.0	266	9	HSHLADR13	X82239 H.sapiens H
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c	40	19	100.0	266	9	HUMMHDRB1I	L78167 Human MHC c
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c	44	19	100.0	266	9	AF352291	AF352291 Homo sapi
c	45	19	100.0	266	9	AF352295	AF352295 Homo sapi

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RESULT   1
US-08-025-038-42/c
; Sequence 42, Application US/08025038
; Patent No. 5545526
;  GENERAL INFORMATION:
;    APPLICANT:  BAXTER-LOWE, Lee-Ann
;    TITLE OF INVENTION:  Method For HLA Typing
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  777 E. Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53202-5367
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/025,038
;      FILING DATE:  19930301
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/544,218
;      FILING DATE:  27-JUN-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Meyers, Philip G.
;      REGISTRATION NUMBER:  30,478
;      REFERENCE/DOCKET NUMBER:  204 854
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (414)289-3761
;      TELEFAX:  (414)289-3791
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  282 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  unsure
;      LOCATION:  1..13
US-08-025-038-42


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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 cacgtcgctgtcgaagcgtgcgtactcctc 30
           ||||||||||||||||||||||||||||||
Db     132 CACGTCGCTGTCGAAGCGTGCGTACTCCTC 103


RESULT   2
US-08-025-038-43/c
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GAGGAGTACGCACGCTTCGACAGCGACGTG

; Sequence 43, Application US/08025038
; Patent No. 5545526
; GENERAL INFORMATION:
;   APPLICANT: BAXTER-LOWE, Lee-Ann
;   TITLE OF INVENTION: Method For HLA Typing
;   NUMBER OF SEQUENCES: 46
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 777 E. Wisconsin Avenue
;   CITY: Milwaukee
;   STATE: Wisconsin
;   COUNTRY: USA
;   ZIP: 53202-5367
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/025,038
;   FILING DATE: 19930301
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/544,218
;   FILING DATE: 27-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Meyers, Philip G.
;   REGISTRATION NUMBER: 30,478
;   REFERENCE/DOCKET NUMBER: 204 854
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (414)289-3761
;   TELEFAX: (414)289-3791
; INFORMATION FOR SEQ ID NO: 43:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 282 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-025-038-43

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  Best Local Similarity 100.0%; Pred. No. 0.00023;
  Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 132 CACGTCGCTGTCGAAGCGTGCGTACTCCTC 103

RESULT 3
US-08-025-038-44/c
; Sequence 44, Application US/08025038
; Patent No. 5545526
; GENERAL INFORMATION:
;   APPLICANT: BAXTER-LOWE, Lee-Ann
;   TITLE OF INVENTION: Method For HLA Typing

; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 777 E. Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-5367
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/025,038
; FILING DATE: 19930301
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/544,218
; FILING DATE: 27-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Philip G.
; REGISTRATION NUMBER: 30,478
; REFERENCE/DOCKET NUMBER: 204 854
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414)289-3761
; TELEFAX: (414)289-3791
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-025-038-44

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Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Sequence 45, Application US/08025038
; Patent No. 5545526
; GENERAL INFORMATION:
; APPLICANT: BAXTER-LOWE, Lee-Ann
; TITLE OF INVENTION: Method For HLA Typing
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 777 E. Wisconsin Avenue
; CITY: Milwaukee

```
;       STATE:  Wisconsin
;       COUNTRY:  USA
;       ZIP:  53202-5367
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/025,038
;       FILING DATE:  19930301
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/544,218
;       FILING DATE:  27-JUN-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meyers, Philip G.
;       REGISTRATION NUMBER:  30,478
;       REFERENCE/DOCKET NUMBER:  204 854
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (414)289-3761
;       TELEFAX:  (414)289-3791
;   INFORMATION FOR SEQ ID NO:  45:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  282 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-025-038-45


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Db     132 CACGTCGCTGTCGAAGCGTGCGTACTCCTC 103


RESULT   5
US-08-025-038-46/c
; Sequence 46, Application US/08025038
; Patent No. 5545526
;  GENERAL INFORMATION:
;    APPLICANT:  BAXTER-LOWE, Lee-Ann
;    TITLE OF INVENTION:  Method For HLA Typing
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  777 E. Wisconsin Avenue
;      CITY:  Milwaukee
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53202-5367
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/025,038
;       FILING DATE:  19930301
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/544,218
;       FILING DATE:  27-JUN-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Meyers, Philip G.
;       REGISTRATION NUMBER:  30,478
;       REFERENCE/DOCKET NUMBER:  204 854
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (414)289-3761
;       TELEFAX:  (414)289-3791
;   INFORMATION FOR SEQ ID NO:  46:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  282 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-025-038-46


  Query Match             100.0%;  Score 30;  DB 1;  Length 282;
  Best Local Similarity   100.0%;  Pred. No. 0.00023;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 cacgtcgctgtcgaagcgtgcgtactcctc 30
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Db     132 CACGTCGCTGTCGAAGCGTGCGTACTCCTC 103
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RESULT 10
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LOCUS HSU26659 262 bp DNA linear PRI 26-JAN-1999
DEFINITION Human MHC Class II HLA DRB1 gene, exon 2, partial cds.
ACCESSION U26659
VERSION U26659.1 GI:4096271
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 262)
AUTHORS Brautbar,C., Israel,S., Safirman,C. and Smith,A.G.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-1995) Chaim Brautbar, Tissue Typing Laboratory,
Hadassah Medical Organization, Kiryat Hadassah, PO Box 12000,
Jerusalem il-91120, Israel
FEATURES Location/Qualifiers
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BASE COUNT 57 a 65 c 94 g 46 t
ORIGIN

Query Match 100.0%; Score 22; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cgtttcctgtggcagcctaaga 22
||||||||||||||||||||||
Db 3 CGTTTCCTGTGGCAGCCTAAGA 24

SID 192

244-262 - SID 222 in same seq.

07106102

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=> fil reg; d que l3
FILE 'REGISTRY' ENTERED AT 13:10:32 ON 13 MAY 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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STRUCTURE FILE UPDATES:   12 MAY 2002  HIGHEST RN 414355-21-8
DICTIONARY FILE UPDATES:  12 MAY 2002  HIGHEST RN 414355-21-8

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

Crossover limits have been increased.  See HELP CROSSOVER for details.

Calculated physical property data is now available.  See HELP PROPERTIES
for more information.  See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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                CAGGGUAACUUCUUUA|UAAAGAAGUUACCCUGCCUCGCCCACGCCA/SQSN
L3           18 SEA FILE=REGISTRY ABB=ON  L2 AND SQL<100


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CN   GenBank AX268628 (9CI)  (CA INDEX NAME)
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SEQ      1 ctgcactgtg aagctctcac
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HITS AT:   2-20

L3   ANSWER 2 OF 18  REGISTRY  COPYRIGHT 2002 ACS
RN   383679-85-4  REGISTRY
CN   GenBank AX001204 (9CI)  (CA INDEX NAME)
SQL  20

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HITS AT:   2-20

L3   ANSWER 3 OF 18  REGISTRY  COPYRIGHT 2002 ACS
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CN   GenBank AR053221 (9CI)  (CA INDEX NAME)
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HITS AT:   2-20

L3   ANSWER 4 OF 18  REGISTRY  COPYRIGHT 2002 ACS
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CN   GenBank AR053214 (9CI)  (CA INDEX NAME)
SQL  20

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SQL  20

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HITS AT:    2-20

L3   ANSWER 6 OF 18  REGISTRY  COPYRIGHT 2002 ACS
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CN   GenBank AR051223 (9CI)  (CA INDEX NAME)
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L3   ANSWER 7 OF 18  REGISTRY  COPYRIGHT 2002 ACS
RN   383679-80-9  REGISTRY
CN   GenBank AR020498 (9CI)  (CA INDEX NAME)
SQL  20

SEQ      1 ctgcactgtg aagctctcac
            ========= ==========
HITS AT:    2-20

L3   ANSWER 8 OF 18  REGISTRY  COPYRIGHT 2002 ACS
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CN   GenBank AR097014 (9CI)  (CA INDEX NAME)
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HITS AT:    19-37

L3   ANSWER 9 OF 18  REGISTRY  COPYRIGHT 2002 ACS
RN   367840-53-7  REGISTRY
CN   GenBank AR097013 (9CI)  (CA INDEX NAME)
SQL  69

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                                                 ===== ==========

        51 tgcagcggcg agttgagcc
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HITS AT:    36-54

L3   ANSWER 10 OF 18  REGISTRY  COPYRIGHT 2002 ACS
RN   351119-12-5  REGISTRY
CN   GenBank AR152020 (9CI)  (CA INDEX NAME)
SQL  75

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HITS AT:    52-73

L3   ANSWER 11 OF 18  REGISTRY  COPYRIGHT 2002 ACS
RN   222656-99-7  REGISTRY
CN   GenBank AR020491 (9CI)  (CA INDEX NAME)
SQL  20
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SEQ 1 ctgcactgtg aagctctcac
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HITS AT: 2-20

L3 ANSWER 12 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 195184-75-9 REGISTRY
CN GenBank A42459 (9CI) (CA INDEX NAME)
SQL **23**

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NTE doublestranded

L3 ANSWER 13 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 188420-65-7 REGISTRY
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OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(G-C-T-G-C-A-C-T-G-T-G-A-A-G-C-T-C-T-C-A-C)
SQL **21**

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L3 ANSWER 14 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 186078-36-4 REGISTRY
CN GenBank I28140 (9CI) (CA INDEX NAME)
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L3 ANSWER 15 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 170835-89-9 REGISTRY
CN DNA, d(A-C-G-T-T-T-C-C-T-G-T-G-G-C-A-G-C-C-T-A-A-G-A-G-G) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(A-C-G-T-T-T-C-C-T-G-T-G-G-C-A-G-C-C-T-A-A-G-A-G-G)
SQL **25**

SEQ 1 acgtttcctg tggcagccta agagg
========= ========== ===
HITS AT: 2-23
NTE singlestranded

L3 ANSWER 16 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 154216-89-4 REGISTRY
CN DNA, d(C-C-G-C-T-G-C-A-C-T-G-T-G-A-A-G-C-T-C-T-C-A-C) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-C-G-C-T-G-C-A-C-T-G-T-G-A-A-G-C-T-C-T-C-A-C)
SQL **23**

SEQ 1 ccgctgcact gtgaagctct cac
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HITS AT: 5-23
NTE singlestranded

L3 ANSWER 17 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 146049-88-9 REGISTRY
CN Cytidine, 2'-deoxycytidylyl-(3'.fwdarw.5')-thymidylyl-(3'.fwdarw.5')-2'-deoxyguanylyl-(3'.fwdarw.5')-2'-deoxycytidylyl-(3'.fwdarw.5')-2'-deoxyadenylyl-(3'.fwdarw.5')-2'-deoxycytidylyl-(3'.fwdarw.5')-thymidylyl-(3'.fwdarw.5')-2'-deoxyguanylyl-(3'.fwdarw.5')-thymidylyl-(3'.fwdarw.5')-2'-deoxyguanylyl-(3'.fwdarw.5')-2'-deoxyadenylyl-(3'.fwdarw.5')-2'-deoxyadenylyl-(3'.fwdarw.5')-2'-deoxyguanylyl-(3'.fwdarw.5')-2'-deoxycytidylyl-(3'.fwdarw.5')-thymidylyl-(3'.fwdarw.5')-2'-deoxycytidylyl-(3'.fwdarw.5')-thymidylyl-(3'.fwdarw.5')-2'-deoxycytidylyl-(3'.fwdarw.5')-2'-deoxyadenylyl-(3'.fwdarw.5')-2'-deoxy- (9CI) (CA INDEX NAME)
SQL **20**

SEQ 1 ctgcactgtg aagctctcac
========= ==========
HITS AT: 2-20
NTE singlestranded

L3 ANSWER 18 OF 18 REGISTRY COPYRIGHT 2002 ACS
RN 143864-42-0 REGISTRY
CN DNA, d(C-G-C-T-G-C-A-C-T-G-T-G-A-A-G-C-T-C-T-C-A-C-C-A) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-G-C-T-G-C-A-C-T-G-T-G-A-A-G-C-T-C-T-C-A-C-C-A)
SQL **24**

SID 3/2
SEQ 1 cgctgcactg tgaagctctc acca
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HITS AT: 4-22
NTE singlestranded

FILE 'CAPLUS' ENTERED AT 13:10:52 ON 13 MAY 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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FILE COVERS 1907 - 13 May 2002 VOL 136 ISS 20
FILE LAST UPDATED: 10 May 2002 (20020510/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L4 10 L3

=> d ibib ab hitrn l4 1-10; fil hom

L4 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:790760 CAPLUS
DOCUMENT NUMBER: 132:217605
TITLE: High-resolution typing for HLA-DRB1*15 and -DRB1*16 by fluorescence-marked sequence-specific priming (TaqMan assay)
AUTHOR(S): Tremmel, M.; Opelz, G.; Mytilineos, J.
CORPORATE SOURCE: Department of Transplantation Immunology, University of Heidelberg, Heidelberg, D-69120, Germany
SOURCE: Tissue Antigens (1999), 54(5), 508-516
CODEN: TSANA2; ISSN: 0001-2815
PUBLISHER: Munksgaard International Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Sequence-specific primed polymerase chain reaction (PCR-SSP) is widely used in HLA labs. The TaqMan method, which is described here for high-resoln. typing of HLA-DRB1*15 and -DRB1*16, does not require elaborate and time-consuming post-PCR detection steps. In this one-tube assay, conventional PCR-SSP and fluorescence detection of the amplicon with a doubly labeled fluorescent probe are combined: a fluorogenic hybridization probe (FHP) labeled with a spectral resolvable fluorescent reporter dye (FAM or TET) at its 5' terminus and a common quencher dye (TAMRA) at its 3' terminus is cleaved by the 5' nuclease activity of Taq DNA polymerase only if the target sequence is amplified. An increase of fluorescence intensity indicates a successful amplification. For high-resoln. typing of HLA-DRB1*15 and -DRB1*16 alleles we designed two FHPs and 14 specific primer mixes (7 for DR15 and 7 for DR16). Amplification of the specific sequence was detected by a FAM-labeled FHP, whereas amplification of the internal control was detected by a TET-labeled FHP. We were able to type all heterozygous DRB1*15/DRB1*16 subtype combinations. For evaluation, 60 HLA-DRB1*15-pos. and 40 HLA-DRB1*16-pos. individuals were typed and the results were compared with conventional PCR-SSP DR15/16 subtyping. There were no discrepancies between the two methods. The TaqMan method is an alternative to conventional PCR-SSP typing which is suitable for routine use in HLA labs.
IT **146049-88-9**
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(3' PCR primer 15021; high-resoln. typing for HLA-DRB1*15 and -DRB1*16 by fluorescence-marked sequence-specific priming (TaqMan assay))
REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:246558 CAPLUS
DOCUMENT NUMBER: 131:125988
TITLE: Fluorotyping of HLA-DRB by sequence-specific priming and fluorogenic probing
AUTHOR(S): Albis-Camps, M.; Blasczyk, R.
CORPORATE SOURCE: Department of Internal Medicine, Division of Hematology and Oncology, Blood Bank, Virchow-Klinikum, Humboldt-University, Berlin, Germany
SOURCE: Tissue Antigens (1999), 53(3), 301-307
CODEN: TSANA2; ISSN: 0001-2815
PUBLISHER: Munksgaard International Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Similar to the recently described HLA-A and -C fluorotyping strategies, the aim of this study was to develop a sequence-specific primed polymerase chain reaction (PCR-SSP)-based fluorotyping method for HLA-DRB. Applying the fluorogenic 5' nuclease assay, it is possible to increase the sample

pca probably 102(a) date & ref.

throughput rate by abolishing all labor-intensive post-amplification steps. Addnl., problems related to contamination are eliminated. The method relies on the 5'-3' exonuclease activity of the Taq-DNA Polymerase which cleaves a target-specific and individually labeled fluorogenic probe during successful PCR. Different labeled probes specific for different targets can be applied in a single PCR, allowing independent detection of the specific HLA and the internal control product. The probe used to detect the HLA-DRB specific amplicons was labeled at its 5' end with FAM as the reporter and further 3' with TAMRA as the quencher. The probe hybridized within the 2nd exon to a conserved region which was covered by all primer mixes. In case of amplification, the cleavage of the fluorogenic probe led to an interruption of the TAMRA-mediated quenching effect and generated a significant increase of the FAM fluorescence. The HLA-DRB fluorotyping information was based on the FAM fluorescence released by 24 individual primer mixes. A TET-TAMRA-labeled probe was used to indicate amplification of the internal control sequence in each PCR reaction. So far, 170 PCR typed clin. samples representing all serol. defined HLA-DRB specificities were analyzed using this fluorotyping method. The results were 100% concordant with those obtained by conventional agarose gel detection.

IT **146049-88-9**

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(PCR primer; fluorotyping of HLA-DRB by sequence-specific priming and fluorogenic probing)

REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:34808 CAPLUS

DOCUMENT NUMBER: 130:91257

TITLE: A method for determining the histocompatibility locus antigen class II

INVENTOR(S): Blasczyk, Rainer

PATENT ASSIGNEE(S): Biotest A.-G., Germany

SOURCE: Eur. Pat. Appl., 36 pp.
CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 887423	A1	19981230	EP 1997-110438	19970626
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
EP 892069	A2	19990120	EP 1998-111696	19980625
EP 892069	A3	19990331		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: EP 1997-110438 19970626

AB The present invention relates to methods and materials for detg. the HLA Class II type of a subject, wherein group-specific sequences are used to design primer mols. which may be used in amplification protocols which accurately identify the HLA group(s) and/or allele(s) carried by the subject. Thus, group-specific sequence motifs, which include sequences of intron 1, were found in HLA DRB genes. These motifs were used to design PCR primers which are useful in detg. HLA type of subjects.

IT **146049-88-9**

RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)

(DRB20AS PCR primer; method for detg. histocompatibility locus antigen

class II)
REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:222969 CAPLUS
DOCUMENT NUMBER: 126:234120
TITLE: HLA-DRB1*04 high resolution typing
AUTHOR(S): Bouwens-Rombouts, A.G.M.; Verduyn, W.; Versluis, L.F.; Schreuder, G.M.Th.; Tilanus, M.G.J.; Giphart, M.
CORPORATE SOURCE: Department of Pathology, Section Molecular Pathology, University Hospital, Utrecht, NL-3508 GA, Neth.
SOURCE: Exp. Clin. Immunogenet. (1997), Volume Date 1996, 13(2), 84-91
CODEN: ECIME4; ISSN: 0254-9670
PUBLISHER: Karger
DOCUMENT TYPE: Journal
LANGUAGE: English
AB High resoln. typing for HLA-DR4 is required to identify the individual subtypes. In this study a panel of DR4-pos. samples was typed by both sequencing-based typing (SBT) and oligohybridization (PCR sequence-specific oligonucleotide; PCR-SSO). SBT reveals the highest resoln.; moreover, ambiguous DRB1*04 allelic combinations can be resolved by a selective amplification of the individual alleles and subsequent sequencing. An extended DR4-specific PCR-SSO makes high resoln. typing possible; however, an addnl. protocol is required to resolve ambiguities.
IT **188420-65-7**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (GSAP86(AC) primer; HLA-DRB1*04 high resoln. typing)

L4 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:398161 CAPLUS
DOCUMENT NUMBER: 125:106095
TITLE: HLA class II genotyping by reverse dot blot method. Application to the high-resolution DRB1 typing
AUTHOR(S): Kaneshige, Toshihiko; Uchida, Kiyohisa
CORPORATE SOURCE: Diagnostic Science Department, Shionogl and Co., Ltd., Osaka, Japan
SOURCE: MHC, Major Histocompat. Complex (1994), 1(Suppl.), 159-163
CODEN: MMHCFQ
DOCUMENT TYPE: Journal
LANGUAGE: English
AB High resoln. HLA-DRB1 genotyping using the reverse dot blot method is described. In the reverse dot blot method dT-tailed sequence-specific oligonucleotide probes (SSOPs) are immobilized onto a membrane, and PCR products are hybridized to these SSOPs in a single reaction.
IT **146049-88-9D**, biotin-labeled
RL: ARG (Analytical reagent use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses) (PCR primer; HLA-DRB1 genotyping by PCR and reverse dot blot hybridization)

L4 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:388722 CAPLUS
DOCUMENT NUMBER: 125:77682
TITLE: A rapid HLA-DRB1*04 subtyping method using PCR and DNA heteroduplex generators
AUTHOR(S): Savage, D. A.; Tang, J. P.; Wood, N. A. P.; Evans, J.; Bidwell, J. L.; Wee, J. L. K.; Oei, A. A.; Hui, K. M.
CORPORATE SOURCE: Institute Molecular and Cell Biology, National University Singapore, Singapore
SOURCE: Tissue Antigens (1996), 47(4), 284-292

CODEN: TSANA2; ISSN: 0001-2815
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We describe here a rapid polymerase chain reaction (PCR)-based method for the identification of HLA-DRB1*0401-*0412 alleles. The method is based on the generation of specific DNA heteroduplex patterns between PCR products derived from selective group-specific amplification of the various DRB1*04 alleles and PCR products derived from two synthetic DNA heteroduplex generator (DHG) mols. following non-denaturing polyacrylamide minigel electrophoresis. One DHG was designed to detect DRB1*0401, *0405, *0407, *0408, and *0409 alleles, while the other was designed to detect DRB1*0402, *0403, *0404, *0406, *0410, *0411, and *0412 alleles. Characteristic heteroduplex patterns were obtained for all DRB1*04 alleles tested both in homozygous and heterozygous situations. Both DHG and PCR-SSP (sequence-specific primer) typing were performed on 41 DRB1*04 pos. DNAs from Singaporean Chinese blood donors and complete concordance in results was obtained. HLA-DRB1*0403, *0405, and *0406 were found to account for 95% of the DRB1*04 alleles in the population studied. The DHG technique described is tech. simple and rapid since it essentially involves only two PCR amplifications per individual subtyping. The technique is particularly useful for resolving DRB1*04 combinations which are indistinguishable by PCR-SSO (sequence-specific oligonucleotide) or PCR-SSP subtyping.

IT **146049-88-9**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; rapid HLA-DRB1*04 subtyping method using PCR and DNA heteroduplex generators)

L4 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1995:792435 CAPLUS
DOCUMENT NUMBER: 123:332222
TITLE: Allele-specific HLA-DRB1 amplification of forensic evidence samples with mixed genotypes
AUTHOR(S): Allen, Marie; Saldeen, Tom; Gyllensten, Ulf
CORPORATE SOURCE: Biomedial Center, University Uppsala, Uppsala, Swed.
SOURCE: BioTechniques (1995), 19(3), 454-6, 458, 460-3
CODEN: BTNQDO; ISSN: 0736-6205
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A major problem in analyzing forensic casework samples is the presence of genetic material from more than one individual in the material evidence. For instance, in sexual assault cases the evidence (vaginal swabs) usually contains a majority of vaginal epithelial cells and varying amts. of sperm cells from the perpetrator. Samples with mixed genotypes are also common among other biol. evidence materials such as nail scrapes and mixed bloodstains. We have developed an allele-specific amplification system for the highly polymorphic HLA class II DRB1 locus that permits the detection of individual alleles in a sample with mixed genotypes, independent of the initial frequency of the alleles. Using a set of eight allele-specific amplification primers and typing the amplified fragments with sequence-specific probes, most of the 60 DRB1 alleles can be resolved. The method is highly specific and sensitive, with the potential for amplifying 15 copies of a particular allele in a background of 3 x 105 copies of other alleles. The method was successfully applied to three forensic cases, where the material evidence consisted of sperm stains on panties, nail scrapes and bloodstains on skin. Thus the DRB1 allele-specific amplification system can be employed for the unambiguous detn. of the presence of individual alleles in materials suspected to contain mixed genotypes, even when the alleles of interest constitute only a small fraction of the total DNA.

IT **170835-89-9**
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST

(Analytical study); BIOL (Biological study); USES (Uses)
(PCR primer; allele-specific HLA-DRB1 amplification of forensic evidence samples with mixed genotypes)

L4 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:209581 CAPLUS
DOCUMENT NUMBER: 120:209581
TITLE: Rapid DNA typing for class II HLA antigens: Subtyping of DRw52-associated DRB1 alleles
AUTHOR(S): Horne, C.; Keown, P. A.
CORPORATE SOURCE: B.C. Transplant Soc., BC, Can.
SOURCE: Tissue Antigens (1993), 41(5), 243-8
CODEN: TSANA2; ISSN: 0001-2815
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Serol. typing for MHC class II antigens is incapable of identifying important subtypes for certain DRB1 alleles and occasionally leads to errors of assignment, particularly with the DR antigens assocd. with DRw52. To simplify DNA typing of DRw52-assocd. DRB1 alleles, a new rapid method was developed using PCR-RFLP. The PCR-RFLP method is based on allele-specific amplification followed by digestion of PCR-amplified DNA with restriction enzymes. Group-specific amplification of the second exon of DR3, DR5, DR6 and DR8 was achieved using a 5' primer specific for the first hypervariable region sequence common to all alleles in this group and generic 3' primers. Human genomic DNA was amplified in a Perkin-Elmer Thermocycler. The presence of a 265-bp fragment was confirmed by agarose gel electrophoresis. Restriction enzyme digestion using RsaI followed by PAGE gave a pattern unique for some alleles and placed the remainder in subgroups. Digestion of the PCR product with one or two of the following enzymes (Asp 700, HaeII, MnlI, MboII, KspI, and HphI) permitted the identification of 21 of the 22 alleles. DRB1*1103 and DRB1*1104 are not distinguished by this method and can be distinguished by SSOP (sequence-specific oligonucleotide probes) or by using a specific 3' primer. For some heterozygous combinations, addnl. primers are used to provide full subtyping. This method provides a rapid and less costly alternative to PCR-SSOP for DRw52 subtyping in the smaller lab. as only one amplification is required (2 primers) for the majority of samples. The patterns produced by restriction digest are easy to interpret and complete subtyping using 3 addnl. primers can be accomplished in <2 days. This method should significantly improve the selection of unrelated donors for bone marrow or solid organ transplantation and facilitate immunogenetic studies in autoimmune diseases.
IT **154216-89-4**
RL: USES (Uses)
(PCR primer 3'GT, for antigen HLA-Drw52-assocd. DRB1 alleles subtyping by RFLP anal.)

L4 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:510546 CAPLUS
DOCUMENT NUMBER: 119:110546
TITLE: PCR primers and hybridization probes for HLA-DR.beta. DNA typing
INVENTOR(S): Erlich, Henry A.; Begovich, Ann B.; Bugawan, Teodorica; Griffith, Robert L.; Scharf, Stephen J.; Apple, Raymond J.
PATENT ASSIGNEE(S): Hoffmann-La Roche, F., und Co. A.-G., Switz.
SOURCE: PCT Int. Appl., 86 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 27
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9210589	A1	19920625	WO 1991-US9294	19911206
W: AU, CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, MC, NL, SE				
AU 9191361	A1	19920708	AU 1991-91361	19911206
AU 656161	B2	19950127		
EP 514534	A1	19921125	EP 1992-902641	19911206
EP 514534	B1	19980401		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
AT 164630	E	19980415	AT 1992-902641	19911206
ES 2115667	T3	19980701	ES 1992-902641	19911206
US 5567809	A	19961022	US 1993-50073	19930422

PRIORITY APPLN. INFO.:
US 1990-623098 A2 19901206
US 1986-839331 B2 19860313
US 1986-899344 B1 19860822
US 1990-491210 B2 19900309
WO 1991-US9294 A 19911206

AB Amplification and detection methods, generic and allele- or group-specific amplification primers, nonisotopic sequence-specific oligonucleotide probes, including probes for identifying previously unknown alleles at the DRB1 locus, and kits for practicing the methods, are described. The invention provides a rapid, simple, and precise system for typing the HLA-DRB alleles, including those that cannot be distinguished by serolog. methods.

IT **143864-42-0**
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(hybridization probe for HLA-DR.beta. DNA typing)

L4 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:95184 CAPLUS
DOCUMENT NUMBER: 118:95184
TITLE: Identification of the HLA-DRB1*04, -DRB1*07, and -DRB1*09 alleles by PCR amplification with sequence-specific primers (PCR-SSP) in 2 hours
AUTHOR(S): Zetterquist, Henrik; Olerup, Olle
CORPORATE SOURCE: Cent. BioTechnol., Karolinska Inst., Huddinge, Swed.
SOURCE: Hum. Immunol. (1992), 34(1), 64-74
CODEN: HUIMDQ; ISSN: 0198-8859
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The clin. applicability of genomic HLA class II typing techniques has increased after the introduction of PCR-based typing strategies. In typing by PCR amplification using sequence-specific primers (PCR-SSP), amplification of specific alleles or groups of alleles is achieved, provided that the mismatch(es) of the SSP is located in the 3' end of the primer. Thus, the specificity of the typing system becomes part of the amplification step, which reduces the total typing time to a min. by simplifying the postamplification processing of samples. The set of primers presented here identifies all of the alleles of the DR4 group, DRB1*0401-DRB1*0411, as well as the DRB1*07 and DRB1*0901 alleles. In the present study of DR4 alleles, PCR-SSP was compared with hybridization with sequence-specific oligonucleotide probes following group-specific PCR amplification (PCR-SSO). The two typing strategies gave completely concordant results in the 90 DR4-pos. and the 32 DR4-neg. individuals and cell lines studied. DR7,DQ9/DR9,DQ9 discrimination using PCR-SSP, was compared with MspI DQA RFLP typing, also with concordant results in the 33 DR7- and/or DR9-pos. and 36 DR7- and DR9-neg. individuals and cell lines tested. No false-neg. or false-pos. typing results were obtained. Genomic typing by PCR-SSP was performed in the overall time of 2 h, including rapid DNA prepn., PCR amplification, postamplification processing, documentation, and interpretation of results. This makes the

PCR-SSP strategy for HLA class II typing attractive not only in population- and disease-assocn. studies, but also in routine clin. practice, including donor-recipient matching prior to cadaveric transplantation.

IT **146049-88-9**

RL: USES (Uses)

(as DNA primer for polymerase chain reaction, for antigen HLA-DR .beta. chain gene HLA-DRB1 allele typing)

FILE 'HOME' ENTERED AT 13:11:07 ON 13 MAY 2002

RESULT 5
S40633
LOCUS S40633 690 bp DNA linear PRI 06-MAY-1993
DEFINITION HLA class II: DPA1 (DPA1*0101) [human, Genomic, 690 nt].
ACCESSION S40633
VERSION S40633.1 GI:1679890
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 690)
AUTHORS Marsh,S.G. and Bodmer,J.G.
TITLE HLA class II nucleotide sequences, 1991
JOURNAL Immunogenetics 33 (5-6), 321-334 (1991)
MEDLINE 91267561
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 40633] from the original journal article.
This sequence comes from Figure 15.
COMMENT On Nov 21, 1996 this sequence version replaced gi:1619630.
Region: HLA class II.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .690
/gene="DPA1"
/allele="DPA1*0101"
BASE COUNT 150 a 195 c 189 g 156 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db    253 GATCCCCCTGAGGTGACCGTG 273
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SID 27

RESULT 1
S63210
LOCUS S63210 106 bp DNA linear PRI 25-AUG-1993
DEFINITION DQB1 (DQB1*0301)=HLA class II antigen {exon 2} [human, bone marrow donor D1, Genomic, 106 nt].
ACCESSION S63210
VERSION S63210.1 GI:386472
KEYWORDS .
SOURCE human bone marrow donor D1.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 106)
AUTHORS Spurkland,A., Knutsen,I., Markussen,G., Vartdal,F., Egeland,T. and Thorsby,E.
TITLE HLA matching of unrelated bone marrow transplant pairs: direct sequencing of in vitro amplified HLA-DRB1 and -DQB1 genes using magnetic beads as solid support
JOURNAL Tissue Antigens 41 (3), 155-164 (1993)
MEDLINE 93303754
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 134478] from the original journal article. This sequence comes from Fig. 4.
FEATURES Location/Qualifiers
source 1. .106
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1. .106
/partial
/gene="DQB1"
/note="HLA class II antigen"
/allele="DQB1*0301"
BASE COUNT 19 a 34 c 26 g 23 t 4 others
ORIGIN

Query Match 100.0%; Score 30; DB 9; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 cacgtcgctgtcgaagcgtgcgtactcctc 30
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Db      15 CACGTCGCTGTCGAAGCGTGCGTACTCCTC 44
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RESULT 11
HSZ75044/c
LOCUS HSZ75044 171 bp DNA linear PRI 06-AUG-1996
DEFINITION H.sapiens HLA-DQB1 gene.
ACCESSION Z75044
VERSION Z75044.1 GI:1483518
KEYWORDS histocompatibility complex; HLA class II gene; HLA-DQB1 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 171)
AUTHORS Sittisombut,N.
TITLE Polymorphism of selected HLA class II genes in northern Thais
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 171)
AUTHORS Sittisombut,N.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1996) Sittisombut N., Faculty of Medicine, Chiang
Mai University, Microbiology, 110 Suthep Street, Chiang Mai,
Thailand, 50200
FEATURES Location/Qualifiers
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